

FIFTH *FALCIPARUM* GENOME MEETING

June 30th-1st July, Hinxton, UK

Remarkable progress in sequencing the genome of the *Plasmodium falciparum* malarial parasite was reported at a recent meeting held at Hinxton Hall, Cambridgeshire, UK. The meeting brought together investigators from UK and US sequencing centres participating in the '*falciparum* genome project'. This project is supported by a consortium of funding agencies and is an excellent example of a collaborative, coordinated approach, by both scientists and funders, to achieve a large-scale scientific objective (for further details see *Parasitology Today*, 14, 342-344, 1998).

Technical challenges posed by the AT rich genomes of *Plasmodium* species had raised significant doubts as to the feasibility of the *falciparum* project at its initiation in 1996. These doubts, however, now seem a long way behind as researchers at the Hinxton meeting reported that sequencing of chromosomes 2 and 3 is nearly complete. Shotgun cloning of chromosomes 1 and 4 is finished and it is anticipated that sequencing of these will be at the closure stage by next February. Cloning of chromosomes 5-9 and 12-14 is underway. A further significant technical advance has been the development of an optical mapping technique by Professor David Schwartz of New York University that is now enabling high resolution mapping of the *falciparum* genome in a time-scale that was previously inconceivable.

The Hinxton meeting was the fifth in a series of regular meetings that provide an opportunity for researchers and funders participating in the sequencing consortium not only to report on progress, but to share experiences and to plan strategies for efficient exploitation of sequence information. The meeting gave particular consideration to ensuring full accessibility of data to the wider malaria research community through establishing optimally designed database systems. Plans were also put in place for computer-based tutorials on 'accessing and analysing genome data' to be held at a number of meetings during 1998; the aim being to raise awareness of the considerable opportunities offered by the genome project and to encourage 'mining' of data by scientists in a wide range of disciplines.

Presentations at the meeting demonstrated that analysis of accumulating sequence data is already beginning to provide important insights into the unusual properties of the *falciparum* genome and its encoded proteins. Researchers involved in other sequencing projects, such as the yeast genome project, also provided valuable input on effective approaches for using genome information, based on their experiences in moving from sequence data to functional analysis of genes and proteins, including the use of microarray technology. A series of workshops were proposed to allow in depth consideration of specific aspects of the *falciparum* genome project, such as database development and drug and vaccine discovery.

A full report on the meeting will be posted on the internet shortly. The next meeting will be held 29 January 1999 in Washington DC, USA.